GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Result
No.
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Maximum DB seq length: 2000000000
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Perfect score
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                               12 7 7 93 . 5 5 6 7 . 5 7 7 5 6 7 . 5 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 5 6 7 . 
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4.215 Million cell updates/sec
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032A 032A 1764 1NE		39.55 39.55 39.55 39.55 39.55 39.55
A-764 ZA-764		44444444
A. 764 A. Application US/08487032A PORMATION: TO DOIGLS SMITH INVENTION: RELATING TO HELLOBACTER PYLORI FOR INVENTION: RELATING TO HELLOBACTER PYLORI FOR INVENTION: DIACNOSTICS AND THERAPEUTICS SEB: LAHIVE & COCKFIELD SEB: LAHIVE & COCKFIELD BOSTON MASSACRUSELTS WISA 02109-1875 READABLE FORM: TYPE: Ploppy disk RE: IBM PC compatible RE: PLOPPY disk RE: IBM PC compatible RE: PC-DS/MS-DOS RE: PatentIn Release #1.0, Version #1.25 APPLICATION DATA: ATION NUMBER: US/08/487,032A DATE: 07-JUNE-1995 AREDICATION NUMBER: 36,07 NCE/DOCKET NUMBER: 36,07		υυυυυυυυυυυ ωω
cation US/08487032A N: LAS SMITH ON: NUCLEIC ACID A ON: NUCLEIC ACID A CES: 880 DDRESS: HIVE & COCKFIELD ate Street husetts PC Compatible PC Compatible PC COMPATION: DATA: PC-DOS/MS-DOS PORMITION: DATA: PC-DOS/MS-DOS PORMATION: TIN UNMER: GTN-001 N INFORMATION: 01-JUMBER: 36,207 UMBER: 47,001 URBER: 47,001 UR		231 233 233 1193 1193 278 278 213
m US/0848 MITH MITH RELATING B80 S: & COCKFIE treet ts ts ts M: COCKFIE TOS/MS Release ATA: US/08/4 MBER: GT ORMATION: 136,207 MBER: GT ORMATION: 17-7400 100: 764: 17591 1.in LSAVLSSSL		
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TELEFAX: (617)227-594 INFORMATION FOR SEQ ID NO:

(617) 227-5941

833:

(617) 227-7400

TELEPHONE:

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                                                                                                                                                                                                   TELEFAX: (617)227-594
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 325 amino acid
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LENGTH: 264 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                       NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36.207
REFERENCE/DOCKST NUMBER: GTI
TELECOMMUNICATION INFORMATION:
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                                                                         HYPOTHETICAL:
ORIGINAL SOURCE
                                                                                       TOPULCE. TYPE: pro
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ATTORNEY/AGENT INFORMATION:
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                 FEATURE:
NAME/KEY:
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                                                      ORGANISM:
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(617) 227-5941
NO: 498:
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Best Local Similarity
Matches 32; Conserv
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                                                                        Matches
                                                                                                        Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                  MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,03
                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: GT
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: LAHIVE & COCKFIELD
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TITLE OF INVENTION:
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                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 1...560
OTHER INFORMATION: /note= "vacuolating cytotoxin"
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                                                                                         Local
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289 KNNVWATGVGGASFISGGTXTLYGINXGYDRFIK----
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Similarity 25.9%;
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                                                                    Score 55.5; DB 1;
Pred. No. 3.2;
9; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTN-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 64; DB : Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Length 264,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
                                                                    23;
                                                                                                        Length 560;
                                                                        Indels
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 -GVIVGGYAAÝGYS 335
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                                                                      Gaps
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RESULT 7 US-08-487-032A-632

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US-08-487-032A-473
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Best Local Similarity
                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617)227-594
INFORMATION FOR SEQ ID NO:
                                                                                                                              FEATURE: FEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: 1...1178
OTHER INFORMATION: /note= "cytotoxicity associatedimmunodominant antigen [H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Va
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,032A
FILING DATE: 07-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
ORGANISM: Hel
                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1178 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Mandragourae, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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CORRESPONDENCE ADDRESS:
                                                                    Local Similarity
                                                                                                                                                                                                                            ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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745 GINPEWISKVENLNAALNEFKNGKNKDFSKVTQAKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 RLTNIADPRTFEPNMLTYG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                 71 GTNINWHSKY--ANGALNGF--GLNVGYKKFFQFKS 102
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                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                : (617)27-5941
(617)227-5941
NO: 473:
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                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                    linear
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                                                                                    6.1%;
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20.3%; Pred. No.
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                                                                                  Score 49;
Pred. No.
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                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.25
                                                                                                   DB 1; Length 1178;
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 780
                                                                    Indels
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RESULT 11

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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: GT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
NFORMATION FOR SEQ ID NO: 663:
                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                           APPLICANT: DOUGLAS SMITH TITLE OF INVENTION: NUCLE TITLE OF INVENTION: RELATITIES OF INVENTION: DIAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,032A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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LENGTH: 214 amino acid
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ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                    STATE: Mar
                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 5.8%; Score 46; DB 1; Length 214; Local Similarity 46.2%; Pred. No. 8.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 GLNVELQINPEVKDFFTFKSISTTNK 154
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                                                                                                                                       02109-1875
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                                                                                                                                                                              Massachusetts
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                                                                                                                                                                                                                 3: LAHIVE & COCKFIELD 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 amino acids
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                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                           NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS
US/08/487,032A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
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RESULT 15
US-08-487-032A-573
US-08-487-032A-573
; Sequence 573, Applicat.
; GENERAL INFORMATION:
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Search completed: April 29, 2004, 14:59:58 Job time : 4 secs
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Best Local Similarity 20.2
Matches 24; Conservative
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prote
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207 REFERENCE/DOCKET NUMBER: GTT TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FORM PC compatible
COMPUTER: PATENT PC COMPATION
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: US/08/487,032A
FILING DATE: 07-UNE-1995
ATTORNEY/AGENT INFORMATION:
ANAME. MAGAZEGUESE AND PROPERTY OF THE PROPERTY OF THE PARTY OF THE 
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature LOCATION: 1...308
OTHER INFORMATION: /not OTHER INFORMATION: [Vik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                      172 APLNTPVZASADGIVDFVKTRSNAGYGNLVRIEHAFGFSSIYTHLDHVNVQPKSFIQKGQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 GLFDYGHADLGKQVYAPNKIQLDMVSWGVGSI 147
                                                                                                                                                                      232 LI----GYSGKSGNSGGEKLHYEVRFLGKILDAEKFLAWDLDHFQSALEENKFIEWKNL 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 PTFN---
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                                                                                                                                                                                                                                     55 VVGCPPGLTANKHNPGGTNINWH------SKYANGALNGFGLNVGYKKFFQFKSL 103
                                                                                                                                                                                                                                                                                                                                                                                                   15 AVLSSSLLAEGDGV--YIGTNYQLGQARL-----NSNIYNTGDCT------GS 54
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(7) TO NO: 573:
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